

Supplementary Table S1. Domains in polyvalent proteins

Domain [Number of proteins containing the domain]	Predicted function	Phyletic profile	Notes
<b>Enzymatic domains</b>			
Metallopeptidases (MPTase) [3618]	Protease	archaea, euryarchaeota, nanoarchaeota, acidobacteria, actinobacteria, aquificae, armatimonadetes, bacteroidetes, chlamydiae, chloroflexi, chrysiogenetes, cyanobacteria, deferribacteres, deinococci, firmicutes, fusobacteria, planctomycetes, alpha-,beta-,gamma-, delta-, epsilon-proteobacteria, spirochaetes, synergistetes, tenericutes, verrucomicrobia, phages	See main text for more details
Assemblin [5]	Protease	Alpha-, beta- proteobacteria	Found in polyvalent proteins of prophages. See main text.
DD-Peptidase [2]	Protease	Alpha-proteobacteria, phages	Likely to be involved in cellwall metabolism
LonC [1]	Protease	Euryarchaeota	A single instance
Pol $\beta$ family nucleotidyltransferase (NTase/PoIB_NTase) [106]	Protein modification	firmicutes, alphaproteobacteria	See main text for more details
ADP- Ribosyltransferases (ART) [273]	Protein modification	euryarchaeota, bacteroidetes, firmicutes, planctomycetes, alpha-,beta-,gamma-, delta- proteobacteria, spirochaetes, synergistetes, verrucomicrobia, phages	See main text for more details
GCN5-like NH2 acetyltransferase (GNAT) [83]	Protein modification	firmicutes, alpha-,beta-,gamma- proteobacteria, phages	See main text for more details
Kinase [12]	Protein modification	bacteroidetes, chlamydiae, verrucomicrobia	See main text for more details
Formyl transferase [2]	Protein modification?	Beta-proteobacteria	Two instances

Novel Methylase [1]	Protein modifying?	firmicutes	Single instance, not a DNA methylase
DNA adenine methylase (N6A-methylase) [2021]	DNA modification	euryarchaeota, actinobacteria, bacteroidetes, cyanobacteria, deinococci, firmicutes, fusobacteria, planctomycetes, alpha-,beta-,gamma-, delta-, epsilon, proteobacteria, spirochaetes, synergistetes, tenericutes, verrucomicrobia, phages	See main text for more details
DNA Cytosine methylase (DCM) [5]	DNA modification	Actinobacteria, chloroflexi proteobacteria, phages	Found in polyvalent proteins, with no strong neighborhoods, but closer to those derived from (pro)phages.
SNF2-like helicase [1701]	DNA remodeling	euryarchaeota, actinobacteria, bacteroidetes, chloroflexi, cyanobacteria, deinococci, firmicutes, fusobacteria, planctomycetes, proteobacteria, alpha-,beta-,gamma-, delta-, epsilon, proteobacteria, spirochaetes, synergistetes, tenericutes, verrucomicrobia, caudoviruses	Two major families. See main text for more details
Strawberry notch (Sno)-like SWI2/SNF2 ATPase [9]	DNA remodeling	firmicutes, beta-, gamma-proteobacteria	Found mostly in polyvalent proteins of conjugative elements. Always fused to its C-terminal WHTH
SFI helicase [1]	DNA remodeling	chlamydiae	
MCM (DUF927/PF06048) [26]	DNA remodeling/Replicative helicases	Alpha-, beta-, gamma-, deltaproteobacteria	Found in polyvalent proteins of conjugative elements usually fused to the primase
UvrD-like SFI helicase [15]	DNA remodeling	actinobacteria	About 15 instances, mostly co-occurs with a SNF2-like ATPase. See main text for more details
SMS/RadA [33]	Resolving recombination intermediates	bacteroidetes	Found in conjugative elements

ddRB-ParB [1180] ParB [91]	Nuclease/ATPase	actinobacteria, bacteroidetes, chloroflexi, firmicutes alpha,beta-,gamma-, delta-, -epsilon, proteobacteria, spirochaetes, verrucomicrobia, phages	At least 2 distinct families of ParB domains. The most common is the ddrB-like family and the second closer to the classical ParBs. Often present in multiple tandem copies in the same polypeptide. See main text for more details
HNH [1]	Nuclease	betaproteobacteria	Single instance
Relaxase [1]	DNA processing/Nuclease	synergistetes	Found in a single polyvalent protein of conjugative

			elements. A common gene neighbor
Inorganic pyrophosphatase (InPase) [281]	Nucleotide synthesis/signaling	bacteroidetes, cyanobacteria, alpha-, beta-, gamma-, delta-proteobacteria, spirochaetes, phages, caudoviruses	OB fold nucleotide dependent pyrophosphatase. See main text for more details
Phosphoribosyltransferase (PRTase) [61]	Nucleotide synthesis/signaling	firmicutes, beta-, delta-, gamma-proteobacteria, verrucomicrobia, phages, caudoviruses	See main text for more details
RelA/SpoT-like nucleotidyltransferase [350]	ppGpp synthetase/nucleotidyltransferase	euryarchaeota, actinobacteria, bacteroidetes, chlamydiae, cyanobacteria, firmicutes, beta-, delta-, gamma-,epsilon-proteobacteria, spirochaetes, synergistetes, phages	See main text for more details
GGDEF [1]	Signaling	firmicutes	Single occurrence. No clear association
NUDIX [4]	Nucleotide processing	actinobacteria, alpha-, gammaproteobacteria	Only four instances
NADAR (pfam08010/ Phage GP30.3) [5]	Nucleotide processing or RNA processing	firmicutes	Found in polyvalent proteins associated with firmicutes conjugative elements.
NADase/ NTox31 [1]	Nucleotide processing/base clipping enzyme	Alpha-proteobacteria	A single instance
RNA polymerase [62]	Transcription	bacteria, alpha-,gamma-proteobacteria, phages	Only in Roseophages and relatives. See main text for more details
DNAG-like Toprim fold primase [705]	Primase	actinobacteria, bacteroidetes, deferribacteres, firmicutes, fusobacteria, alpha-,beta,gamma-, delta-proteobacteria	Toprim fold primase. See main text for more details

Primpol [33]	Primase	actinobacteria, firmicutes, fusobacteria	RRM fold primase. See main text for more details.
RadC [117]	Processing nucleic acids	euryarchaeota, actinobacteria, bacteroidetes, firmicutes, fusobacteria, alpha-,beta,gamma-, delta-proteobacteria, spirochaetes	See main text for more details
PBECR1 [786]	RNase	bacteroidetes, firmicutes, alpha,beta-,gamma-, delta-, epsilon proteobacteria, spirochaetes, verrucomicrobia, phages	See main text for more details
PBECR2 [260]	RNase	bacteroidetes, beta-,epsilon-proteobacteria, spirochaetes, phages	See main text for more details
PBECR3 [634]	RNase	Euryarchaeota, bacteroidetes, deinococci, firmicutes, fusobacteria, alpha-,beta,gamma-, delta-proteobacteria,	See main text for more details

		spirochaetes, verrucomicrobia, phages	
PBECR4 [169]	RNase	firmicutes, fusobacteria	See main text for more details
PBECR5 [85]	RNase	bacteroidetes, firmicutes, beta,gamma- proteobacteria	See main text for more details
MuF-C [1172]	RNase	actinobacteria, bacteroidetes, firmicutes, nitrospirae, , alpha-,beta-,gamma-, delta-proteobacteria, spirochaetes, synergistetes, verrucomicrobia, phages	The classical Phage MuF Cterminus appears to be inactive. Found in polyvalent proteins of both conjugative elements and phages/prophages. See main text for more details.
2H-phosphoesterase [19]	RNase	actinobacteria, bacteroidetes, chloroflexi, planctomycetes, delta-proteobacteria	See main text for more details
RelE [3]	RNase	Gamma-proteobacteria	Present in polyvalent proteins of conjugative elements.
ToxN [1]	RNase	firmicutes	Present in a polyvalent protein probably derived from of a conjugative element
Lysozyme [72]	Peptidoglycan hydrolysis	firmicutes, alpha-,beta-,gamma, delta- proteobacteria, phages	Also includes Pfam Glucosaminidases. See main text for more details
SpoIID [7]	Peptidoglycan hydrolysis	Alpha-proteobacteria, phages	A distinct alpha-helical enzymatic domain

Zeta-toxin [5]	Cell wall modification	Beta-, gamma- proteobacteria, verrucomicrobia, phages	See main text for more details. Found in polyvalent proteins of both conjugative elements and prophages/phages
Terminase Large Subunit [4]	Packaging	Gamma-, epsilon-proteobacteria	P-loop ATPase involved in packaging DNA
Phage_integrase [7]	DNA Integration	actinobacteria, firmicutes, gamma-proteobacteria	Only seen in polyvalent proteins of conjugative elements
ParA [2]	DNA partitioning	firmicutes	P-loop NTPase
CcdA [1]	Anti-toxin	Gamma-proteobacteria	A single instance in a conjugative element type polyvalent protein
LPD3 [241]	Predicted Enzyme	bacteroidetes, chrysiogenetes, firmicutes, alpha-,beta-, gamma-, delta, epsilon-proteobacteria, spirochaetes, synergistetes, phages	Alpha+beta domain with a conserved C-terminal Y and possibly a H. Secondary structure arrangement is very BECR-like. Found in polyvalent proteins of both conjugative elements and phages/prophages
LPD5 [514]	Predicted enzyme	bacteroidetes, chrysiogenetes, firmicutes, alpha-, beta-, delta-, gamma- proteobacteria, phages	An alpha+beta domain almost always found Nterminal to the Metallopeptidase domain with conserved D, K, R, R residues. There might be two domains in this too.
LPD15 [50]	Predicted enzyme	firmicutes	An alpha+beta domain with a highly conserved HYE motif and other polar residues.

			Always seen at the Nterminus of polyvalent proteins of conjugative elements
LPD19 [166]	Predicted enzyme	firmicutes	An alpha+beta domain with a highly conserved cysteine in a CxE motif. Predicted to be enzymatic. Associated with polyvalent proteins of firmicute conjugative elements.

LPD21 (DUF3849/ PF12960) [138]	Predicted enzyme	firmicutes	An alpha+beta domain with highly conserved D and R residues possibly enzymatic. Associated with polyvalent proteins of firmicute conjugative elements
LPD22 [160]	Predicted enzyme	firmicutes, alpha-, beta-, delta-, gamma-proteobacteria synergistetes, phages	Alpha-helical domain with highly conserved aspartate residues. Found in both phage/prophage contexts. Often in the neighborhood of a lysozyme gene.
LPD34 [76]	Predicted enzyme	firmicutes	An alpha+beta domain with a large, prominent helix with conserved E. Several additional conserved residues suggests potential enzymatic function, including conserved HTxN and SN motifs. Associated with polyvalent proteins of firmicute conjugative elements
LPD39 [82]	Predicted enzyme	Alpha-,beta-,gamma-proteobacteria	An alpha-helical domain with a conserved histidine and two acidic residues. Associations suggest a phage/prophage association
DNA_ligase_A_M [1]	ATP dependent DNA Ligase	Alpha-proteobacteria	DNA ligase
<b>DNA binding domains</b>			
ArdC-N/DUF1738 [2676]	Alpha-helical domain that is likely to bind single stranded DNA	euryarchaeota, nanoarchaeota, bacteria, acidobacteria, actinobacteria, aquificae, armatimonadetes, bacteroidetes, chloroflexi, chrysiogenetes, cyanobacteria, deferribacteres, deinococci, firmicutes, fusobacteria, planctomycetes, alpha-, beta-, gamma-, delta-,epsilon-	See main text for more details. Almost always associated with polyvalent proteins of conjugative elements. Mostly towards the N-terminus, although there can be exception.
		proteobacteria, spirochaetes, synergistetes, tenericutes, phages	

MutS_N-terminal domain/MutS_I [98]	DNA binding	bacteroidetes, firmicutes, gamma-proteobacteria	Alpha+beta DNA binding Nterminal domain that specifically binds mismatched single-stranded regions of DNA See main text for more details. Found in polyvalent proteins of conjugative elements
Histone H-NS like [1]	DNA binding	gammaproteobacteria	Found in a single instance in a prophage-type polyvalent protein
RhoN/SAP [21]	DNA binding	firmicutes, gamma-, deltaproteobacteria	H-E-H fold found in polyvalent proteins of phages/prophages. Often fused to MuF. See main text for more details.
Ftsk_gamma-like HTH [4]	DNA binding	betaproteobacteria	HTH Mainly found in prophage polyvalent proteins.
PriCT2 [54]	DNA binding	Beta-, gamma- proteobacteria	Associated with a Toprim primase and found in context of polyvalent proteins of conjugative elements.
PriCT1 [1]	DNA binding	actinobacteria	One instance in conjugative element polyvalent protein where it is C-terminal to the primpol domain
Zf-CHC2 [124]	DNA binding?	bacteroidetes, firmicutes, fusobacteria	A zinc finger associated with the Toprim Primase, usually at the N-terminus of polyvalent proteins of conjugative elements
Toprim_N [5]	DNA binding?	actinobacteria	Present in polyvalent proteins of conjugative elements N-terminal to the Toprim-primase
SnoC [9]	DNA-binding	firmicutes, beta-, gammaproteobacteria	A wHTH found C-terminal to the Strawberry notch-like SWI2/SNF2 helicase. Found mostly in polyvalent proteins of conjugative elements.
Zinc Ribbon (ZnR) [4]	DNA-binding	Firmicutes, gammaproteobacteria	Present in polyvalent proteins of conjugative elements.
TraJ-like (MobC) Ribbon-Helix-Helix (RHH) [2]	DNA-binding	bacteroidetes, deltaproteobacteria	Present in polyvalent proteins of conjugative elements.
HsdM_N [1]	DNA binding?	bacteroidetes	Usually found N-terminus to the N6A-methylase, but in

			the single instance fused to LPD33.
<b>Predicted structural domains</b>			
DarA-N [296]	Structural domain	Beta-, gamma-proteobacteria, proteobacteria>gammaproteobacteria, phages	An Alpha+beta fold domain with a conserved aspartate, and an asparagine residue followed by a basic residue (Nx+ motif). Mainly found in polyvalent proteins of phages/prophages. hdf, which is a solo version of the domain, and the Phage P1 DarA protein are components of the phage P1 head. Found in polyvalent proteins of phages/prophages
DarA-C [322]	Structural domain	bacteroidetes, firmicutes, gamma-proteobacteria, phages	Largely alpha-helical domain, mainly found in polyvalent proteins of phages/prophages. In Phage P1, the DarA protein is a component of the phage P1 head.
MuF [1681]	Phage head structural component	euryarchaeota, actinobacteria, bacteroidetes, chloroflexi, deinococci, firmicutes, fusobacteria, nitrospirae, alpha-, beta-, gamma, delta, epsilonproteobacteria, spirochaetes, verrucomicrobia, phages	Phage head component. Fused to a variety of domains. Found in prophages/phages
Phage portal [153]	DNA packaging	euryarchaeota, actinobacteria, bacteroidetes, chloroflexi, cyanobacteria, deinococci, firmicutes, planctomycetes, beta-, gamma-proteobacteria, verrucomicrobia, phages	An SH3 fold domain that combines with the Terminase ATPase subunits to package DNA, a critical component of the Terminase-portal packaging system.
Gp129 [3]	Structural protein	bacteroidetes	Present in polyvalent proteins of prophages
PhageT4-gp20 [1]	Structural protein	phages	
Phage_Min_cap2 [2]	Structural protein	firmicutes	Present in polyvalent proteins of prophages
<b>Miscellaneous domains</b>			

ArdA [231]	Restriction inhibition	firmicutes	An alpha+beta domain that mimics DNA and directly binds Restriction enzymes and inhibits their activities. Always found in polyvalent proteins of firmicutes conjugative elements. Usually present towards the N-terminus
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YodL [453]	Interaction with cytoskeleton	firmicutes, fusobacteria	See main text for details. Seen in polyvalent proteins of conjugative elements
CbtA/YeeV [27]	Inhibits polymerization of cytoskeletal proteins	gammaproteobacteria	See text for more details. Always found in polyvalent proteins of conjugative elements
SpoVG [19]	Nucleic acid binding	firmicutes	Always fused to LPD26 in polyvalent proteins of conjugative elements
Pentapeptide repeats [5]	scaffolding	firmicutes	Found in polyvalent proteins of conjugative elements
Heat Repeats [1]	Scaffolding	betaproteobacteria	One occasion, in a prophagelike polyvalent protein
YvbH [2]	Scaffolding?	Beta-proteobacteria	Mediates protein oligomerization
DnaJ [43]	chaperone	bacteroidetes, firmicutes, spirochaetes	Mainly found in polyvalent proteins of conjugative elements. Always N-terminal to LPD29 in this set of proteins.
BID [2]	Uncharacterized	beta-, gamma-proteobacteria	
KfrB [1]	Uncharacterized	Gamma-proteobacteria	Alpha+beta domain present in polyvalent proteins of conjugative element. Widely seen in the neighborhood of conjugative elements. KfrB domain has been speculated to play a role in discrimination of self from non-self in plasmid conjugation systems.
AIRS [1]	Uncharacterized	Alpha-proteobacteria	Found in a polyvalent protein of a conjugative element
AIRS_C [1]	Uncharacterized	Alpha-proteobacteria	Found in a polyvalent protein of a conjugative element

LPD1 [708]	Uncharacterized	actinobacteria, bacteroidetes, chrysiogenetes, firmicutes, alpha-,beta-, gamma-, delta-proteobacteria, spirochaetes, tenericutes, phages	Third most common LPD. Small alpha helical domain with a conserved ExxARxxE motif. Short and hence not suspected to be enzymatic. Found in polyvalent proteins of both conjugative elements and phages/prophages
LPD2 (Overlap with DUF4316/ PF14195) [411]	Uncharacterized	firmicutes, fusobacteria	three conserved acidic residues and a hNN motif. Found in polyvalent proteins of conjugative elements
LPD4 [67]	Uncharacterized	bacteroidetes, firmicutes, , alpha-,beta-, gamma-, deltaproteobacteria, synergistetes, phages	NxxRD motif. Found in polyvalent proteins of phages/prophages
LPD6 [592]	Uncharacterized	actinobacteria, bacteroidetes, cyanobacteria, firmicutes, fusobacteria, , alpha-,beta-, gamma-, delta-, epsilonproteobacteria, spirochaetes, verrucomicrobia, viruses	Short mostly alpha-helical domain with conserved basic and tryptophan residues. Found in polyvalent proteins of conjugative elements
LPD7 (formerly PTox1 in Osa paper) [168]	Uncharacterized	Beta-, gamma-proteobacteria	With conserved D and F residues. Widely present in polyvalent proteins and gene neighborhoods of conjugative elements.
LPD8 (DUF3560/ PF12083) [573]	Uncharacterized	actinobacteria, bacteroidetes, cyanobacteria, firmicutes, fusobacteria, alpha-,beta-, gamma-, delta-proteobacteria, verrucomicrobia, phages	Alpha helical domain with conserved basic residues. Mainly found in polyvalent proteins of conjugative elements.
LPD9 [52]	Uncharacterized	bacteroidetes, firmicutes, alpha-, gamma-proteobacteria, phages	Alpha-helical domain with conserved N and F residues. Found in polyvalent proteins of phages/prophages
LPD10 [1]	Uncharacterized	actinobacteria	Short alpha-helical domain. Single instance
LPD11 [31]	Uncharacterized	actinobacteria, firmicutes	Short alpha-helical domain with conserved hydrophobic residues. Found in polyvalent proteins of conjugative elements
LPD12 [90]	Uncharacterized	bacteroidetes, cyanobacteria, firmicutes, alpha-,beta-, gamma-, delta-proteobacteria, phages	Alpha+beta domain. Mainly found in polyvalent proteins of conjugative elements and a few in phages

LPD13 [7]	Uncharacterized	bacteroidetes, gammaproteobacteria, spirochaetes	Alpha+beta domain. Found in both polyvalent proteins of conjugative elements and phages/prophages
LPD14 [23]	Uncharacterized	bacteroidetes, firmicutes	Alpha-helical domain with a conserved E. Mainly found in polyvalent proteins of prophages.
LPD16 [240]	Uncharacterized	firmicutes, fusobacteria, spirochaetes	Alpha+beta domain with a characteristic conserved G. Mainly found in polyvalent proteins of conjugative elements.
LPD17 [232]	Uncharacterized	firmicutes	Mostly alpha-helical domain with a conserved D and W.

			Mainly found in polyvalent proteins of conjugative elements.
LPD18 [151]	Uncharacterized	firmicutes	Mostly all beta domain with conserved acidic residues. Mainly found in polyvalent proteins of conjugative elements.
LPD20 [71]	Uncharacterized	firmicutes	Central beta-rich domain bookended by alpha-helices. Mainly found in polyvalent proteins of conjugative elements.
LPD23 [69]	Uncharacterized	bacteroidetes, firmicutes, alpha,beta-, gamma-, delta-, epsilonproteobacteria, phages	Short alpha-helical domain that is usually N-terminal to an MPTase. Might be an extension. Found in both in polyvalent proteins of conjugative elements and phages/prophages, but more in the latter.
LPD24 [1]	Uncharacterized	firmicutes	Short all-beta domain with limited distribution. Mainly in polyvalent proteins of conjugative elements
LPD25 [477]	Uncharacterized	chloroflexi, firmicutes, fusobacteria, gammaproteobacteria, tenericutes	Alpha+beta domain found in polyvalent proteins of conjugative elements.

LPD26 [84]	Uncharacterized	firmicutes	Small alpha-helical domain with two conserved acidic residues in the loop between two helices. Mainly found in polyvalent proteins of conjugative elements
LPD27 [108]	Uncharacterized	firmicutes	Small beta-beta-alpha-beta domain with striking HHxS-D motif. Found in polyvalent proteins of conjugative elements
LPD28 [20]	Uncharacterized	firmicutes	Fast diverging, largely beta domain lacking strongly conserved polar residues. Found in polyvalent proteins of conjugative elements
LPD29 [70]	Uncharacterized	bacteroidetes, firmicutes, alpha, gamma-proteobacteria, spirochaetes	An alpha+beta domain with conserved polar residues. Found in polyvalent proteins of conjugative elements. Often fused to DnaJ, LPD6 and LPD29
LPD30 [15]	Uncharacterized	Alpha-, gamma-proteobacteria	Alpha+beta domain with a conserved E. Found in

			polyvalent proteins of conjugative elements.
LPD31 (DUF2958/PF11171) [255]	Uncharacterized	actinobacteria, bacteroidetes, firmicutes, fusobacteria, alpha-, beta-, gamma-proteobacteria, spirochaetes	Alpha+beta domain with conserved polar residues. Mostly found in polyvalent proteins of conjugative elements.
LPD32 [535]	Uncharacterized	firmicutes, fusobacteria, spirochaetes	Second most common LPD. Alpha+beta domain that may be found in multiple tandem copies. Found in polyvalent proteins of conjugative elements
LPD33 [98]	Uncharacterized	euryarchaeota, actinobacteria, bacteroidetes, firmicutes, alpha-, delta-, gamma- proteobacteria	Small helical domain that is also seen in classical type I RM systems, where it is fused at the C-terminus of the HsdR (nuclease+helicase) component. Found in polyvalent proteins of conjugative elements

LPD35 (overlaps with DUF1249/ PF06853) [26]	Uncharacterized	firmicutes	Mostly all-beta domain mainly found in polyvalent proteins of conjugative Solo versions appear to cooccur in gene neighborhoods with NUDIX.
LPD36 [1821]	Uncharacterized	actinobacteria, bacteroidetes, cyanobacteria, deinococci, firmicutes, fusobacteria, planctomycetes, alpha-,beta-, gamma-, delta-, epsilonproteobacteria, spirochaetes, synergistetes, tenericutes, verrucomicrobia, phages	The most commonly found LPD. Largely helical domain bookended by reasonably well-conserved N and a nucleotide binding G-patch. Also has a well-conserved GxG motif. Almost always found in methyltransferasehelicase architecture and found in polyvalent proteins of both conjugative elements and phages/prophages.
LPD37 [13]	Uncharacterized	bacteroidetes, alpha-, betaproteobacteria, verrucomicrobia	Alpha+beta domain with conserved D and RR motifs. Found in polyvalent proteins that are likely to be phage/prophage-derived.
LPD38 [46]	Uncharacterized	bacteroidetes, firmicutes, alpha,beta-, gamma-proteobacteria, phages	Alpha+beta domain. Found in polyvalent proteins of phages/prophages.
LPD40 [125]	Uncharacterized	firmicutes	Conserved tandem acidic residues (D- motif). Found in polyvalent proteins of conjugative elements.
DUF3275/ PF11679 [1]	Uncharacterized	Gamma-proteobacteria	Found in polyvalent proteins of a conjugative element
DUF960/ PF06124 [1]	Uncharacterized	firmicutes	
DUF1156/ PF06634 [2]	Uncharacterized	spirochaetes	
DUF4262/ PF14081 [3]	Uncharacterized	actinobacteria	
DUF3631/ PF12307 [4]	Uncharacterized	Beta-proteobacteria	Found in polyvalent proteins of a conjugative element
DUF4116/ PF13475 [4]	Uncharacterized	fusobacteria, spirochaetes	Found in polyvalent proteins of a conjugative element
DUF192/ PF02643 [5]	Uncharacterized	chloroflexi	Found in polyvalent proteins of a conjugative element